

# SEQUENCE LISTING

<110> Weintraub, Bruce D.  
Szkudlinski, Mariusz

<120> MUTANTS OF THYROID STIMULATING HORMONE  
AND METHODS BASED THEREON

<130> UOFMD.002C1

<140> PCT US98/19772

<141> 1998-09-22

<150> 60/135,505

<151> 1998-09-17

<150> 08/939,472

<151> 1997-09-22

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 91

<212> PRT

<213> Homo sapiens

<400> 1

Ala	Pro	Asp	Val	Gln	Asp	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu	Asn	Pro
1				5				10						15	
Phe	Phe	Ser	Gln	Pro	Gly	Ala	Pro	Ile	Leu	Gln	Cys	Met	Gly	Cys	Cys
			20					25					30		
Phe	Ser	Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys	Lys	Thr	Met	Leu
			35					40					45		
Val	Gln	Lys	Asn	Val	Ser	Glu	Ser	Thr	Cys	Cys	Val	Ala	Lys	Ser	Tyr
			50					55				60			
Asn	Arg	Val	Thr	Val	Met	Gly	Gly	Phe	Lys	Val	Glu	Asn	His	Thr	Ala
65					70					75					80
Cys	His	Cys	Ser	Thr	Cys	Tyr	Tyr	His	Lys	Ser					
				85						90					

<210> 2

<211> 118

<212> PRT

<213> Homo sapien

<400> 2

Phe	Cys	Ile	Pro	Thr	Glu	Tyr	Thr	Met	His	Ile	Glu	Arg	Arg	Glu	Cys
1				5				10						15	
Ala	Tyr	Cys	Leu	Thr	Ile	Asn	Thr	Thr	Ile	Cys	Ala	Gly	Tyr	Cys	Met
			20					25					30		
Thr	Arg	Asp	Ile	Asn	Gly	Lys	Leu	Phe	Leu	Pro	Lys	Tyr	Ala	Leu	Ser
			35				40					45			
Gln	Asp	Val	Cys	Thr	Tyr	Arg	Asp	Phe	Ile	Tyr	Arg	Thr	Val	Glu	Ile

50	55	60
Pro Gly Cys Pro Leu His Val Ala Pro Tyr Phe Ser Tyr Pro Val Ala		
65	70	75
Leu Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr Ser Asp Cys Ile		80
	85	90
His Glu Ala Ile Lys Thr Asn Tyr Cys Thr Lys Pro Gln Lys Ser Tyr		95
	100	105
Leu Val Gly Phe Ser Val		110
	115	

<210> 3  
 <211> 530  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> CDS  
 <222> (86)...(520)

<400> 3  
 agacaaggca ggggacgcac caaggatgga gatgttccag gggctgctgc tgttgctgct 60  
 gctgagcatg ggcgggacat gggca tcc aag gag ccg ctt cgg cca cgg tgc 112  
 Ser Lys Glu Pro Leu Arg Pro Arg Cys  
 1 5

cgc ccc atc aat gcc acc ctg gct gtg gag aag gag ggc tgc ccc gtg 160  
 Arg Pro Ile Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val  
 10 15 20 25

tgc atc acc gtc aac acc acc atc tgt gcc ggc tac tgc ccc acc atg 208  
 Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met  
 30 35 40

acc cgc gtg ctg cag ggg gtc ctg ccg gcc ctg cct cag gtg gtg tgc 256  
 Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys  
 45 50 55

aac tac cgc gat gtg cgc ttc gag tcc atc cgg ctc cct ggc tgc ccg 304  
 Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro  
 60 65 70

cgc ggc gtg aac ccc gtg gtc tcc tac gcc gtg gct ctc agc tgt caa 352  
 Arg Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln  
 75 80 85

tgt gca ctc tgc cgc cgc agc acc act gac tgc ggg ggt ccc aag gac 400  
 Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp  
 90 95 100 105

cac ccc ttg acc tgt gat gac ccc cgc ttc cag gac tcc tct tcc tca 448  
 His Pro Leu Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser  
 110 115 120

aag gcc cct ccc ccc agc ctt cca agc cca tcc cga ctc ccg ggg ccc 496  
 Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro  
 125 130 135

530

```
<400> 4
tcaatccgc
```

9

[illegible]